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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
10/666,486	09/19/2003	Stewart Shuman	1784/53661-AA	8020

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EXAMINER	
BHAT, NARAYAN KAMESHWAR	
ART UNIT	**PAPER NUMBER**
1634	
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Please find below and/or attached an Office communication concerning this application or proceeding.

The time period for reply, if any, is set in the attached communication.

Office Action Summary	Application No.	Applicant(s)	
	10/666,486	SHUMAN ET AL.	
	Examiner	Art Unit	
	NARAYAN K. BHAT	1634	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on *28 August 2007*.

2a)☐ This action is **FINAL**. 2b)☒ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *45 and 79-100* is/are pending in the application.

4a) Of the above claim(s) _____ is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *45 and 79-100* is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☐ The specification is objected to by the Examiner.

10)☒ The drawing(s) filed on *09 September 2003* is/are: a)☒ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12)☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☐ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____.

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1) ☒ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☒ Information Disclosure Statement(s) (PTO/SB/08) Paper No(s)/Mail Date *12/29/2003*.
4) ☐ Interview Summary (PTO-413) Paper No(s)/Mail Date. _____.
5) ☐ Notice of Informal Patent Application
6) ☐ Other: _____.

DETAILED ACTION

Election/Restrictions

1. This office action is written in reply to Applicant's correspondence filed regarding restriction April 2, 2007, wherein claims 1-44 and 46-78 were cancelled and new claims 80-100 were added.

2. Applicant's election with traverse of invention of group III in the reply filed on April 2, 2007 is acknowledged. The traversal is on the ground(s) that the sequences recited in Figure 11, contain nucleotide sequence "N", wherein "N" represents adenine or thymidine or guanosine or cytosine moieties. Applicant's arguments regarding claims 61 and 62 are moot in view of cancellation of claim 61 and 62. Applicant's argument with regard to claim 79, is found persuasive and the nucleotide restriction requirement regarding claim 79 has been withdrawn.

3. Claims 45 and 79-100 are pending in this application and are under examination.

4. The examiner for this application has changed. Please address future correspondence to Examiner Narayan K. Bhat, Art Unit 1634.

Specification

5. Amendments to the specification and figures to meet the nucleotide sequence and / or amino acid disclosures filed on August 28, 2007 have been reviewed and entered.

Claim Rejections - 35 USC § 112

6. The following is a quotation of the second paragraph of 35 U.S.C. 112:

> The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

7. Claim 79 is rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention.

8. Claim 79 is indefinite over the recitation of "the tag sequences comprises the sequence shown in Figure 11" in lines 7-8, and is confusing because Figure 11 has multiple DNA sequences. It is not clear from the Figure 11, which sequence is encompassed by the claim. Therefore the claim is interpreted broadly to encompass any sequence illustrated in the Figure 11.

Claim Rejections - 35 USC § 102

9. The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

> A person shall be entitled to a patent unless –
>
> (a) the invention was known or used by others in this country, or patented or described in a printed publication in this or a foreign country, before the invention thereof by the applicant for a patent.
>
> (b) the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.

10. Claims 45, 80, 85-89, 91 and 100 are rejected under 35 U.S.C. 102(b) as being anticipated by Kato et al (Gene, 1994, 150, 243-250, This reference was cited in the IDS filed December 29, 2003).

Regarding claim 45, Kato et al teaches a method of obtaining full-length gene sequences comprising: isolating full-length mRNA (Fig. 1B, step 1) and further teaches that poly A RNA contains the cap (pg. 345, column 1, paragraph 2, step 'a' of the claim), which is defined as the full-length RNA in the instant specification (Instant specification, USPGPUB, paragraph 0055). Kato et al also teaches attaching a DNA tag sequence to the isolated mRNA (Fig. 1B, step 3, DNA tag sequence - DNA-RNA chimeric linker, See Fig. 1B legend, pg. 245, column 1, paragraph 2, step 'b' of the claim). Kato et al also teaches synthesizing cDNA using the tagged mRNA as a template (Fig. 1B, step 4, See Fig. 1B legend, pg. 245, column 1, paragraph 3, step 'c' of the claim).

Regarding claim 80, Kato et al teaches that the mRNA is isolated by employing an oligo (dT)- cellulose affinity purification material (pg. 244, column 1, Fig. 1B, legend).

Regarding claims 85 and 86, Kato et al teaches that the mRNA is isolated from animal cells, wherein in the animal cells are human cells (pg. 245, column 1, paragraphs 2 and 3).

Regarding claims 87-89, Kato et al teaches that the mRNA is decapped and dephosphorylated after isolation by enzymatically, wherein the enzyme is a tobacco acid pyrophosphatase (Fig. 1B, enzymes –BAP and TAP, step 1, pg. 245, column 1, paragraph 3).

Regarding claim 91, Kato et al teaches that the mRNA is dephosphorylated using alkaline phosphatase (Fig. 1B, alkaline phosphatase –BAP, pg. 245, column 1, paragraph 3).

Regarding claim 100, Kato et al teaches that the DNA tag sequence attached to the 3' end of the mRNA is a linearized pKA1 expression vector (Fig. 1A, expression vector pKA1, Fig. 1B, Step 3, linearized expression vector- vector primer, See Fig. 1 legend for details).

Claim Rejections - 35 USC § 103

11. The following is a quotation of 35 U.S.C. 103(a) which forms the basis for all obviousness rejections set forth in this Office action:

> (a) A patent may not be obtained though the invention is not identically disclosed or described as set forth in section 102 of this title, if the differences between the subject matter sought to be patented and the prior art are such that the subject matter as a whole would have been obvious at the time the invention was made to a person having ordinary skill in the art to which said subject matter pertains. Patentability shall not be negatived by the manner in which the invention was made.

12. This application currently names joint inventors. In considering patentability of the claims under 35 U.S.C. 103(a), the examiner presumes that the subject matter of the various claims was commonly owned at the time any inventions covered therein were made absent any evidence to the contrary. Applicant is advised of the obligation under 37 CFR 1.56 to point out the inventor and invention dates of each claim that was not commonly owned at the time a later invention was made in order for the examiner to consider the applicability of 35 U.S.C. 103(c) and potential 35 U.S.C. 102(e), (f) or (g) prior art under 35 U.S.C. 103(a).

13. Claims 45, 81-84, 87-88 and 90 are rejected under 35 U.S.C. 103(a) as being unpatentable over Kato et al (Gene, 1994, 150, 243-250) in view of Carninci et al (Genomics, 1996, 37, 327-336, This reference was cited in the IDS filed December 29, 2003).

Claim 84 is dependent from claim 83, which is dependent from claim 80, which is dependent from claim 45. Claims 81 and 82 are dependent from claim 80. Claim 90 is dependent from claim 88, which is dependent from claim 87, which is dependent from claim 45. Teachings of Kato et al regarding claim 45, 80, 87 and 88 are described previously in this office action.

Regarding claims 81-84 and 90, Kato et al are silent about chemical decapping of mRNA and isolation using affinity purification tagged cap structure. However, chemical decapping of mRNA and isolation using affinity purification tagged cap structure were known in the art before the claimed invention was made, as taught by Carninci et al.

Regarding claims 81 and 82, Carninici et al teaches that the mRNA to be isolated comprises biotin moiety (i.e., an affinity purification tag) tagged to cap structure of mRNA (Fig. 1B, see the legend for details, pg. 328, column 1, paragraph 2).

Regarding claims 83-84, Carninci et al teaches that the biotin moiety (i.e., affinity purification material) is captured on magnetic porous particles (i.e., solid support) coated with streptavidin (Fig. 1C, Steps 1-3, See the legend for details, pg. 328, column 2, paragraph 3).

Regarding claim 90, Carninci et al teaches that mRNA is decapped by chemical treatment, wherein the chemical treatment is periodate oxidation (pg. 334, column 1, paragraphs 2 and 3).

Carninci et al also teaches that the oligocapping by RNA ligase produces variable yield and the RNA ligase activity is dependent on the template RNA sequence

and its secondary conformation (pg. 327, column 2, paragraph 3). Carninci et al also teaches that affinity purification of mRNA with tagged cap structure produces high content full length cDNA library with over 95% full length clones with an unbiased representation of the starting mRNA population (Abstract).

It would be have been prima facie obvious to one having the ordinary skill in the art at the time the invention was made to modify the mRNA tagging method of Kato et al with the affinity tagged mRNA cap structure method of Carninci et al.

One having the ordinary skill in the art would have been motivated to modify the mRNA tagging method of Kato et al with a reasonable expectation of success with the expected benefit of producing high content full length cDNA library with over 95% full length clones with an unbiased representation of the starting mRNA population as taught by Carninci et al (Abstract), thus eliminating the use of RNA ligase in the mRNA tagging method of Kato et al.

14. Claims 45, 92-96 and 97 are rejected under 35 U.S.C. 103(a) as being unpatentable over Kato et al (Gene, 1994, 150, 243-250) in view of Shuman (J. Biol. Chem.1994, 269, 2678-32684).

Claims 92-97 are ultimately dependent from claim 45. Teachings of Kato et al regarding claim 45 are described previously in this office action.

Regarding claim 93, Kato et al teaches the DNA tag sequence further comprises a recognition site for EcoR I restriction endonuclease (Fig. 1, See the chimeric linker having EcoR I site).

Regarding claims 92-97, Kato et al is silent about DNA tag sequence having recognition site for vaccinia DNA topisomerase and DNA tag sequence is of double stranded. However, DNA tag sequence having recognition site for vaccinia DNA topisomerase and DNA tag sequence is of double stranded was known in the art before the claimed invention was made as taught by Shuman.

Regarding claims 92 and 94, Shuman teaches a method to generate chimeric DNA molecule and further teaches that the divalent substrate has two recognition sites for type I topoisomerase, wherein type I topoisomerase is vaccinia DNA topoisomerase as defined in instant claim 94 (Abstract, Fig. 2, # S300/301).

Regarding claims 95-97, Shuman teaches an embodiment, wherein the bi-valent substrate comprises the double stranded DNA sequence (Fig. 2, # S300/S301). Shuman further teaches that the bi-valent substrate is 46 base pairs and has two CCCTT recognition sequence for topoisomearase followed by a nucleotide N, wherein N is adenine (Fig. 2, second panel, limitation of claim 96). Shuman also teaches that the bivalent substrate is covalently attached to the topoisomerase (Fig. 3B, lane 5 – without topoisomerase, lane 6, with topoisomerase, pg. 32680, column 1, paragraph 1, limitation of claim 97). The double stranded sequence shown in Fig. 11, has the topoisomerase recognition sequence and is about 40 nucleotide long and attaches to topoisomerase. The bivalent substrate taught by Shuman is broadly interpreted as the nucleotide sequence shown in Figure 11 (limitation of claim 95).

Shuman also teaches that the DNA tag sequence with recognition sequence for topoisomerase cleaves at the recognition site thereby making the tag sequence active

for invitro labeling, ligand tagging and suitable for molecular cloning with reduced concatamer formation and background (pg. 32678, column 2, paragraph 2, pg. 326683, column 2, last paragraph).

It would be have been prima facie obvious to one having the ordinary skill in the art at the time the invention was made to modify the tag sequence of Kato et al with the double strand DNA tag sequence of Shuman.

One having the ordinary skill in the art would have been motivated to modify the tag sequence of Kato et al with a reasonable expectation of success with the expected benefit of having DNA tag sequence with recognition sequence for topoisomerase cleaving at the recognition site thereby making the tag sequence active for invitro labeling, ligand tagging and suitable for molecular cloning with reduced with reduced concatamer formation and background as taught by Shuman (pg. 32678, column 2, paragraph 2, pg. 326683, column 2, last paragraph), thus increasing the repertoire of DNA tag sequence for generating full length cDNA clones in the method of Kato et al.

15. Claims 45, 98 and 99 are rejected under 35 U.S.C. 103(a) as being unpatentable over Kato et al (Gene, 1994, 150, 243-250) in view of Chenchick et al (Biotechniques, 1996, 21, 526-534).

Claim 99 is dependent from claim 98, which is dependent from claim 45. Teachings of Kato et al regarding claim 45 are described previously in this office action.

Regarding claim 98, Kato et al is silent about amplification of the synthesized cDNA with primers comprising the anticoding sequence of the tag sequence at the 5' end and a gene specific sequence at the 3' end.

Regarding claim 99, Kato et al teaches the insertion of the cDNA into an expression vector (Fig. 1, last step).

However, amplification of the cDNA with primers comprising the anticoding sequence of the tag sequence at the 5' end and a gene specific sequence at the 3' end was known in the art at the time of the claimed invention was made as taught by Chenchick et al.

Regarding claim 98, Chenchick et al teaches a method of cloning full length cDNA by ligating adaptors at both ends of the cDNA and selectively amplifying the cDNA by PCR using a combination of adaptor specific primer at the 5' end (i.e., anticoding tag sequence primer at the 5' end) and a gene specific primer at the 3' end (Fig. 1A, adaptor specific primer –AP1, gene specific primer –GSP1, See the legend for details, Abstract).

Chenchick et al also teaches that the Rapid Amplification of cDNA Ends (RACE) is fast, simple and reliable alternative to conventional library screening and well suited for full length cDNA cloning of high medium and low abundant cDNAs up to 9 kbp (pg. 533, column 1, paragraph 3, pg. 534, column 1, paragraph 1).

It would be have been prima facie obvious to one having the ordinary skill in the art at the time the invention was made to modify the cDNA cloning method of Kato et al with the RACE protocol of Chenchick et al.

One having the ordinary skill in the art would have been motivated to modify the cDNA cloning method of Kato et al with a reasonable expectation of success with the expected benefit of having a fast, simple and reliable alternative to conventional library screening method for obtaining full length cDNA clones of 9 kbp long for high medium and low abundant mRNA as taught by Chenchick et al (pg. 533, column 1, paragraph 3, pg. 534, column 1, paragraph 1), thus saving time and cost associated with cDNA library screening method of Kato et al.

16. Claim 79 is rejected under 35 U.S.C. 103(a) as being unpatentable over Kato et al (Gene, 1994, 150, 243-250) in view of Shuman (J. Biol. Chem.1994, 269, 2678-32684) and further in view of Chenchick et al (Biotechniques, 1996, 21, 526-534).

Regarding claim 79, Kato et al teaches a method of obtaining full-length gene sequences comprising: isolating full-length mRNA by employing an oligodT cellulose (i.e., affinity purification material (Fig. 1B, step 1, pg.244, column 1, See Fig. 1B legend for details) Kato et al also teaches that poly A RNA contains the cap (pg. 345, column 1, paragraph 2, step 'a' of the claim), which is defined as the full-length RNA in the instant specification (Instant specification, USPGPUB, paragraph 0055). Kato et al also teaches the decapping and dephoporylating the isolated RNA by bacterial alkaline phosphatase and tobacco acid pyrophosphatase (Fig. 1B, Step 1, BAP and TAP step, See Fig. 1B legend, step 'b' of the claim).

Kato et al further teaches attaching a DNA tag sequence to the decapped dephosporylated mRNA (Fig. 1B, step 3, DNA tag sequence - DNA-RNA chimeric

linker, See Fig. 1B legend, pg. 245, column 1, paragraph 2). Kato et al also teaches synthesizing cDNA using the tagged mRNA as a template (Fig. 1B, step 4, See Fig. 1B legend, pg. 245, column 1, paragraph 3, step'd' of the claim).

Kato et al teaches inserting the synthesized cDNA into an expression vector (Fig. 1B, last step, step 'f' of the claim, see fig. 1A, for details of the expression vector and the legend for the details of the method steps).

Kato et al is silent about DNA tag sequence having recognition site for vaccinia DNA topisomerase and DNA tag sequence is of double stranded. However, DNA tag sequence having recognition site for vaccinia DNA topisomerase and DNA tag sequence is of double stranded was known in the art before the claimed invention was made as taught by Shuman.

Shuman teaches a method to generate chimeric DNA molecule and further teaches that the divalent substrate has two recognition sites for type I topoisomerase, wherein type I topoisomerase is vaccinia DNA topoisomerase as defined in instant claim 94 (Abstract, Fig. 2, # S300/301).

Shuman also teaches an embodiment, wherein the bi-valent substrate comprises the double stranded DNA sequence (Fig. 2, # S300/S301). Shuman further teaches that the bi-valent substrate is 46 base pairs and has two CCCTT recognition sequence for topoisomearase followed by a nucleotide N, wherein N is adenine (Fig. 2, second panel, limitation of claim 96). Shuman also teaches that the bivalent substrate is covalently attached to the topoisomerase (Fig. 3B, lane 5 – without topoisomerase, lane 6, with topoisomerase, pg. 32680, column 1, paragraph 1, limitation of claim 97). The double

stranded sequence shown in Fig. 11, has the topoisomerase recognition sequence and is about 40 nucleotide long and attaches to topoisomerase. The bivalent substrate taught by Shuman is broadly interpreted as the nucleotide sequence shown in Figure 11 (limitation of claim 95).

Shuman also teaches that the DNA tag sequence with recognition sequence for topoisomerase cleaves at the recognition site thereby making the tag sequence active for invitro labeling, ligand tagging and suitable for molecular cloning with reduced concatamer formation and background (pg. 32678, column 2, paragraph 2, pg. 326683, column 2, last paragraph).

It would be have been prima facie obvious to one having the ordinary skill in the art at the time the invention was made to modify the tag sequence of Kato et al with the double strand DNA tag sequence of Shuman.

One having the ordinary skill in the art would have been motivated to modify the tag sequence of Kato et al with a reasonable expectation of success with the expected benefit of having DNA tag sequence with recognition sequence for topoisomerase cleaving at the recognition site thereby making the tag sequence active for invitro labeling, ligand tagging and suitable for molecular cloning with reduced concatamer formation and background as taught by Shuman (pg. 32678, column 2, paragraph 2, pg. 326683, column 2, last paragraph), thus increasing the repertoire of DNA tag sequence for generating full length cDNA clones in the method of Kato et al.

Kato et al and Shuman are silent about amplification of the synthesized cDNA with primers comprising the anticoding sequence of the tag sequence at the 5' end and a gene specific sequence at the 3' end.

However, amplification of the cDNA with primers comprising the anticoding sequence of the tag sequence at the 5' end and a gene specific sequence at the 3' end was known in the art at the time of the claimed invention was made as taught by Chenchick et al.

Chenchick et al teaches a method of cloning full length cDNA by ligating adaptors at both ends of the cDNA and selectively amplifying the cDNA by PCR using a combination of adaptor specific primer at the 5' end (i.e., anticoding tag sequence primer at the 5' end) and a gene specific primer at the 3' end (Fig. 1A, adaptor specific primer –AP1, gene specific primer –GSP1, See the legend for details, Abstract).

Chenchick et al also teaches that the Rapid Amplification of cDNA Ends (RACE) is fast, simple and reliable alternative to conventional library screening and well suited for full length cDNA cloning of high medium and low abundant cDNAs up to 9 kbp (pg. 533, column 1, paragraph 3, pg. 534, column 1, paragraph 1).

It would be have been prima facie obvious to one having the ordinary skill in the art at the time the invention was made to modify the cDNA cloning method of Kato et al and Shuman with the RACE protocol of Chenchick et al.

One having the ordinary skill in the art would have been motivated to modify the cDNA cloning method of Kato et al and Shuman with a reasonable expectation of success with the expected benefit of having a fast, simple and reliable alternative to

conventional library screening method for obtaining full length cDNA clones of 9 kbp long for high medium and low abundant mRNA as taught by Chenchick et al (pg. 533, column 1, paragraph 3, pg. 534, column 1, paragraph 1), thus saving time and cost associated with cDNA library screening method of Kato et al and Shuman.

Double Patenting

17. The nonstatutory double patenting rejection is based on a judicially created doctrine grounded in public policy (a policy reflected in the statute) so as to prevent the unjustified or improper timewise extension of the "right to exclude" granted by a patent and to prevent possible harassment by multiple assignees. A nonstatutory obviousness-type double patenting rejection is appropriate where the conflicting claims are not identical, but at least one examined application claim is not patentably distinct from the reference claim(s) because the examined application claim is either anticipated by, or would have been obvious over, the reference claim(s). See, e.g., *In re Berg*, 140 F.3d 1428, 46 USPQ2d 1226 (Fed. Cir. 1998); *In re Goodman*, 11 F.3d 1046, 29 USPQ2d 2010 (Fed. Cir. 1993); *In re Longi*, 759 F.2d 887, 225 USPQ 645 (Fed. Cir. 1985); *In re Van Ornum*, 686 F.2d 937, 214 USPQ 761 (CCPA 1982); *In re Vogel*, 422 F.2d 438, 164 USPQ 619 (CCPA 1970); and *In re Thorington*, 418 F.2d 528, 163 USPQ 644 (CCPA 1969).

A timely filed terminal disclaimer in compliance with 37 CFR 1.321(c) or 1.321(d) may be used to overcome an actual or provisional rejection based on a nonstatutory double patenting ground provided the conflicting application or patent either is shown to be commonly owned with this application, or claims an invention made as a result of activities undertaken within the scope of a joint research agreement.

Effective January 1, 1994, a registered attorney or agent of record may sign a terminal disclaimer. A terminal disclaimer signed by the assignee must fully comply with 37 CFR 3.73(b).

18. Claims 45, 79-100 are rejected on the ground of nonstatutory obviousness-type double patenting as being unpatentable over claims 1-17 of U.S. Patent No. 6,653,106 in view of Carninci et al (Genomics, 1996, 37, 327-336). Although the conflicting claims are not identical, they are not patentably distinct from each other because of the following reasons.

Regarding instant claims 45 and 79, claim 7 of the patent '106 are drawn to a method of obtaining a cDNA corresponding to a gene, the method comprising: (a) contacting a sequence-specific type I DNA topoisomerase in vitro with a double-

stranded DNA whose first strand is to be covalently joined to an mRNA strand corresponding to the gene, (b) contacting the resulting complex in vitro with a 5'OH-containing mRNA strand corresponding to the gene and having a 5' terminal portion complementary to the 3' terminal portion of the DNA 5' tail, under conditions permitting (i) the mRNA strand to hybridize with the 5' tail and (ii) the topoisomerase to covalently join the mRNA strand and first DNA strand, thereby covalently joining the DNA strand to the mRNA strand; and (c) producing cDNA using as a template the covalently joined mRNA and DNA strands resulting from step (b), thereby obtaining a cDNA corresponding to the gene. Claim 13 of the patent '106 are drawn to a method of generating 5'-OH mRNA by decapping native mRNA. The native mRNA containing the cap is interpreted as full-length mRNA. Claim 45 is obvious over claims 7 and 13 of the patent '106.

Regarding claims 80-84, claims 1-17 of the patent '106 are silent about purification of the mRNA using affinity purification material. However, affinity purification material for the purification of mRNA was known in the art before the claimed invention was made as taught by Carninci et al.

Carninici et al teaches that the mRNA to be isolated comprises biotin moiety (i.e., an affinity purification tag) tagged to cap structure of mRNA (Fig. 1B, see the legend for details, pg. 328, column 1, paragraph 2). Carninci et al also teaches that the biotin moiety (i.e., affinity purification material) is captured on magnetic porous particles (i.e., solid support) coated with streptavidin (Fig. 1C, Steps 1-3, See the legend for details, pg. 328, column 2, paragraph 3). Carninci et al further teaches that mRNA is decapped

by chemical treatment, wherein the chemical treatment is periodate oxidation (pg. 334, column 1, paragraphs 2 and 3).

Carninci et al also teaches that affinity purification of mRNA with tagged cap structure produces high content full length cDNA library with over 95% full length clones with an unbiased representation of the starting mRNA population (Abstract).

It would be have been prima facie obvious to one having the ordinary skill in the art at the time the invention was made to modify the mRNA tagging method of claim 7 of '106 patent with the affinity tagged mRNA cap structure method of Carninci et al.

One having the ordinary skill in the art would have been motivated to modify the mRNA tagging method of claim 7 of '106 patent with a reasonable expectation of success with the expected benefit of producing high content full length cDNA library with over 95% full length clones with an unbiased representation of the starting mRNA population as taught by Carninci et al (Abstract).

Instant claims 85-100 are obvious over claims 2-17 of the patent '106.

Conclusion

19. No claims are allowed.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Narayan K. Bhat whose telephone number is (571)-272-5540. The examiner can normally be reached on 8.30 am to 5 pm.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Ram R. Shukla can be reached on (571)-272-0735. The fax phone number for the organization where this application or proceeding is assigned is 571-273-8300.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see http://pair-direct.uspto.gov. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free). If you would like assistance from a USPTO Customer Service Representative or access to the automated information system, call 800-786-9199 (IN USA OR CANADA) or 571-272-1000.

/Narayan K. Bhat/

Examiner, Art Unit 1634

Narayan K. Bhat, Ph. D.

/BJ Forman/

Primary Examiner, Art Unit 1634